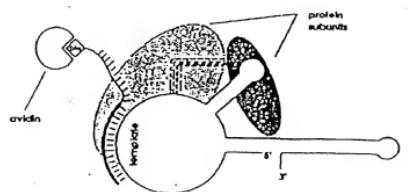


FIGURE 1

PANEL A



PANEL B

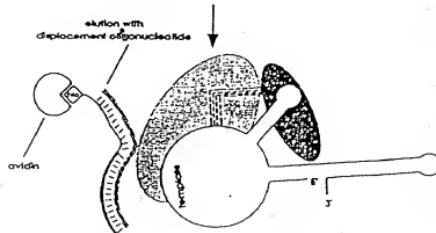
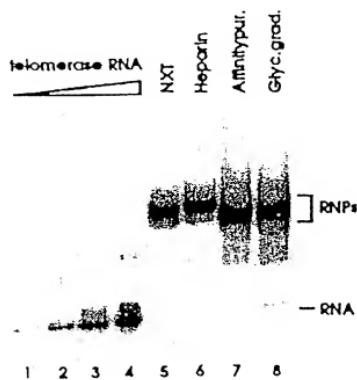
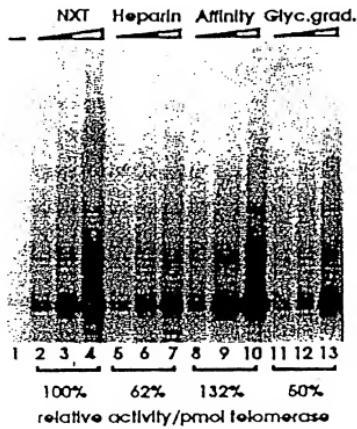


FIGURE 2



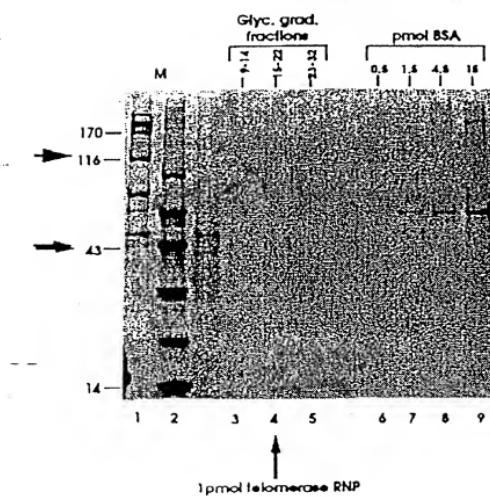
Y067TD-E5259Z60

FIGURE 3



TRIESTO-ESSEZIALE

FIGURE 4



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FIGURE 5

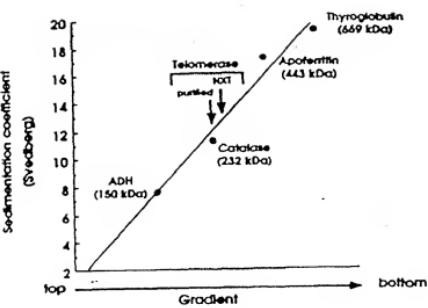


FIGURE 6

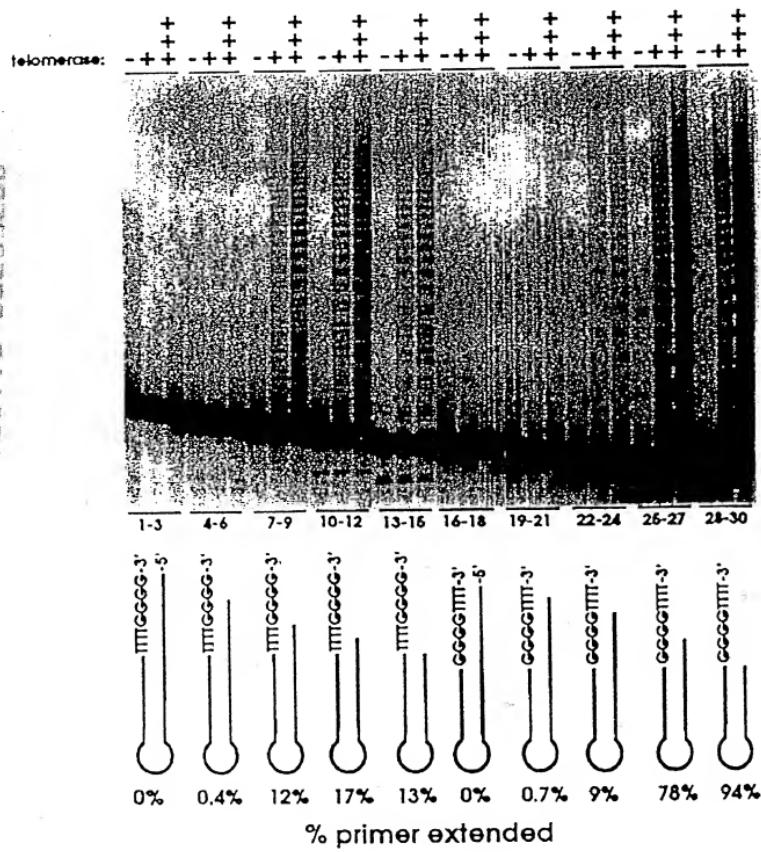


FIGURE 7

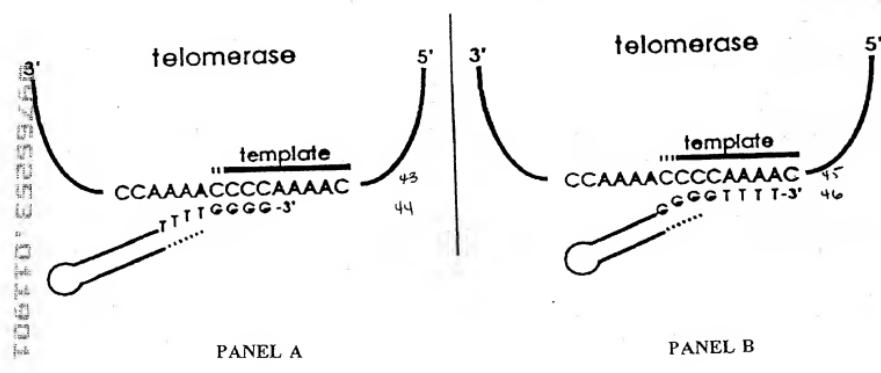


FIGURE 8



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FIGURE 9

1 AAAACCCCAA ACCCCAAAAA CCCCTTTAG AGCCCTGCAG TTGAAATAT
51 AACCTCGATA TTATAAGCT CAGATTAA ATATAATTA CAAAACCTAA
101 ATGGAGGTG ATGTTGATAA TCAAGCTGAT AATCATGGC TTCACTCAGC
151 TCTTAAGACT TGTAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGG
201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTC TTATAAAGAT
251 TTAGAAGATA TTAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG
301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAAA GAAGTATTIT
351 CAACTGGACT AATGATCGAA CCTATTGACA AATGCTTAGT TGAACCTTCTT
401 TCATCAAGCG ATGTTTICAGA TAGACAAAAA CCTTAATGAT TTGGATTTC
451 ACTTAAGGGAA ATCAATTAG CAAAGACCCA TTATTAACA GCTCTTCAA
501 CTCAAAGCA GTATTCCTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
551 ATTGGAAATG AGCTCTCCG ACATCTCTAC ACTAAATATT TAATATTC
601 CGCAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAA AACGTTTTG
651 ATCATTTGAA AGTCACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
701 GCAGACATGA ATGAACTCTCG ATGTTGATCA ACCTGCAAT ACAATGTC
751 GAATGAGAAA GATCAGCTTC TCAACAAACAT CAACGTGCCG AATTGGAATA
801 ATATGAAATC AAGAACAGA ATATTTATTG GCACTCATTT TAATAGAAAT
851 AACCAATTCT TCAAAAAGCA TGAGTTTG AGTAACAAAAA ACAATATTTC
901 AGGGATGGAC AGAGCTCGA CGATATTACG GAATATATTTC AGATTAAATA
951 GAATTAGAAA AAAGCTAAAAA GATAAGGTTA CGAAACAAAT TGCCATAC
1001 CTTGAGAAAG TCAAGATTG TAACCTCAAC TACTATTAA CAAAATTTG
1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAATTC GAAAACTTG
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAGA GCTGTTTACG
1151 TACACAACGT ATAATAAATG CGTCACACAAA TTATTAATG ATTTTTCTA
1201 CAATATACCT CCCAAAGACT TTTTGAETGG AAGAAACCGT AAGAATTTC
1251 AAAAGAAAGT TAAGAAATAT GTGGAACCTAA ACAAGCATGA ACTCATTCA
1301 AAAACATTAT TCGTTGAGAAA GATCAATACA AGAGAAATAT CATGGATGCA
1351 GTTGAGACC TCTGCAAAAGC ATTTTTATTA TTTTGATCAC GAAAACATCT
1401 ACGCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGCTCG
1451 CTGATTAGAT GATTTTCTA TGTCAACCGA CAACAGAAAAA GTTACTCCAA
1501 AACCTTATTAC TACAGAAAAGA ATATTGGGA CGTCATTATG AAAATGTC
1551 TCGCAGACTT AAAGAAGGGAA ACGCTTGTG AGGTCAAGA AAAAGGGTT
1601 GAAGAATGGA AAAAGTCGCT TGGATTGCA CCTGGAAAAC TCAGACTAAT
1651 ACCGAAGGAAA ACTATTCCTC GTCCAAATTAT GACTTCAT AAGAACAGTTG
1701 TAAATTCTAGA CCGGAAGACT ACAAAATTAAT CTACAAATAC GAAGTTATG
1751 AACTCTCACT TAATGCTAA GACATTGAAG AATAGAATGT TTAAAGATCC
1801 TTGGATTTC GCTGTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
1851 AGTTGTTG CAAATGGAAG CAAGTTGGAC AACCAAAATCTTCTTGC
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAACATTC
1951 AACATTCCTA AAAACTACTA ATTACTTTC TTCAGATTC TGGATTATGA
2001 CTGCAAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTGCAAAAC
2051 TTAGAAGA AAGAAATGAA AGATTATTT AGACAGAAAT TCCAGAAGAT
2101 TGCACCTGAA GGAGGACAAAT ATCCAACCTT ATTCACTGTT CTGAAAATG
2151 AACAAATGAA CTAAATGCA AAGAAAACAT TAATTTGTTGA AGCAAGC
2201 AGAAATTATT TTAAGAAGA TAACTTACTT CAACCAAGTC TTAAATATTG
2251 CCAATTAAT TACATTAAC TTAATGGGAA GTTTTATAAA CAAACAAAAG
2301 GAATTCTCA AGGTCTTGA GTTTCATCAA TTTGTCATC ATTATTATTAT

FIGURE 9 (cont.)

2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
2401 CCCTGAAAAT CCAATGTGA ATCTCTTAAT GAGACTTACA GATGACTATC
2451 TTTGATTAC AACTCAAGAG AATAATGCG TATTGTTTAT TGAGAAACTT
2501 ATAACGTAAGTCGTGAAAAA TGGATTAAATGCAATATGA AGAAAATAC
2551 GACTAGTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601 GTGGAGGA GCAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651 TCAATTGATA TGAAAATCT TGCTTTAATG CCAAATATTAA CTTGAGAAAT
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751 CAATGTGGCT CAAGAAGAAA CCAAAGTCGT TTAAATGAA TAACATTACC
2801 CATTATTTA GAAAGACGAT TACAACCGAA GACTTTGCCA ATAAAATCT
2851 CAACAAGTTT TTATATCG GCGGTTACAAATACATGCAA TGAGCCAAG
2901 AATACAAGGA CCACTTAAG AAGAACTTAG CTATGAGCGAT TATGATCGAC
2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001 CCTTGTGC AAATTAAGG ATACAATT TTGGAGAGGAG CATTATCCAG
3051 ACTTTCTCT TAGCACACTG AAGCACTTA TTGAAATATT CAGCACAAAA
3101 AAGTACATT TCAACAGAGT TTGCAATGATC CTCAGGCAA AAGAAGCAA
3151 GCTAAAAGT GACCAATGTC AATCTCTAAAT CCAATATGAT GCATAGTCGA
3201 CTATTCTAAC TTATTTGGA AAGTTAATT TCAATTITG TCTTATATAC
3251 TGGGGTTTGG GGGTTTGGG TTGTTGGGG

FIGURE 10

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHEYKD
51 LEDIKIFAQT NIVATPRDYN EEDFKVIAKR EVFSTGLMIE LIDKCLVELL
101 SSDSVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
151 IGNELFRHLY TKYLIFQRSTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA
201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNNNMKSRTF IFYCTHFNRN
251 NQFFKKHEFV SNKNNISAMD RAQTFITNF RFNRIRKKKL DKVIEKIAYM
301 LEKVVKDFNFN YYLTTKSCPLP ENWRERKKQJ ENLINKTREE KSKYYEELFS
351 YTIDNKCVTQ FINEFFYNIL PKDPLTGRNR KNFQKKVKKY VELNKHELIH
401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKL RWFEDLVVS
451 LIRCFFYVTE QQKSYSKTYY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
501 EEWKKSLGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL
551 NSHMLMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
601 TMDIEKCYDS VNREKLSTFL KTKLSSDF WIMTAQILKR KNNTIVIDSKN
651 FRKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNLDNA KKTLLIVEAKQ
701 RNYFKKDNLQ QPVINICQYN YINFNNGFYK QTKGIPQGLC VSSILSSFYY
751 ATLEESSLGF LRDESMNPEN PVNVNLLMRLT DDYLLITTQE NNAVLFIEKL
801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
851 SIDMKTALM PNINLRIEGI LCTLNLNMQT KKASMWLKKK LKSFLMNNIT
901 HYFRKTITTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID
951 LEVSKIYISV TRAFFKYLV CNIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
1001 KYIFNRVCMI LKAKEAKLKS DQCQSLIQUYD A

FIGURE 11

1 CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAAAGA AAAAATTGAG
51 GTAGTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATGGA
101 TTGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
151 GCTCTTGAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
201 TCGCTTCACT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
251 CTCGGATGCA AATCTTATA ACGATTCCTT CTTGAGAAAA TTAGTTAA
301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTAAATAA
351 AATCAGGTA TGAGGTAT TCTATTTTAT AGATCACTTC TTAAGGAGCA
401 TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTC
451 CCTAGCCAAC AATGATGAGT ATATTAATT CATATGAGAA TGAGTCAG
501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
551 AAAAGGTTTGAATCGAAC AGCAGAAGAAA CTTATTGCTT TTACTATTCG
601 TATGGGTTT ATTACAATG TTITAGGTAT CGACGGTGAAC CTCCGAGTC
651 TTGAGACAAT TGAAAAGCT GTTACAACG GAAGGAATCG CAGTTCTGAA
701 AGTCTGTGATG TGATGCCAT TATTTGTA ATTAACTCA AATATCTTAT
751 CTCATTAA TGATAGCT TAGAAACAAA CCAAAATAAC CATGCAAGT
801 TAATGGATA TA CGTAAAT CTTGGGAC AAATGCACAC TGAATTATA
851 TTGGATTCTT AAAGCATAGA TACACAGAA GCTTTAGAGA CTGATTAGC
901 TTACACAGA TTACCTGTT TGATTACTCT TGCTCATCTC TTATATCTT
951 AAAAGAAGCA GCGGAATGAA AAAGAAGACT AAAGAAGAG ATTCAAAAT
1001 TTGTGATTC TTCTGTAACC GGAATTAAACA ACAAGAATAT TAGCAACGAA
1051 AAAGAAGAG AGCTATCACA ATCCTGATTC TTAAAGATT CAaaaATTCC
1101 AGGTAGAGA GATACATTCA TTAAATTCA TATATTATAG TTTTCATT
1151 CACAGCTGTT ATTTCCTTT ATCTTAACAA TATTTTTGAA TTAGCTGAA
1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTTA CTTAGCTTAT
1251 TCACATTCTAT AGATCGACCT TCATATATCC AATACGATGAA TAAGGAAACA
1301 GCAGTCATCC GTTTAAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
1351 AAGAAAATGGA GCCGAAATCT TAATCAAAA GAATTGCGTC GATATTGCAA
1401 AAGAATCGAA CTCTAAATCT TTGTTAATA AGTATTACCA ATCTTGATTG
1451 ATTGAAAGAGA TTGACGAGGC AACTGACAG AAGATCATTAA AAGAAATAAA
1501 GTAATTITA TTAAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAGTTAG ACAATAAAA
1601 ATACAAACCT TGTCAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA
1651 AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
1701 AAGATTATT TTTCATAA ATTATTGAA AAGAGGGGTT TTGGGGTTT
1751 GGGTTTTGG GG

FIGURE 12

1 CCCCCAAAACCCCAAAACCCATAAAAAAGAAAAATTGAGGTAGTTAGA
 1 GGGGTTTGTGGGTTTGGGTTTGGAATTTCTTTTAACTCCATCAAACT 60

 a P Q N P K T P K P L * K K K K L R * F R -
 b P K T P K P Q N P Y K K R K N C G S L E -
 c P K P Q N P K T P I K K E K I E V V - K -

 61 AAAAAAATATTATCCCCCACAAAATGGAGATGGATATTGATTTGGATGATATAGAAAAATT
 61 TTATTTATAAAGGGCGTGTTCACCTCACCTATAAACCTAACCTATATCTTTAA 120

 a N K I L F P H K W R W I L I W M I * K I -
 b I K Y S R T N G D G Y C F G G Y R K F -
 c * N I I P A Q M E M D I D L D D I K N L -

 121 TACTCTCTAAATCAACAAAGATAGCAGCTCTTGTAGTGACAGAAAAGGATGCAA 180
 121 ATGAAGGATTATGTAAGTTGTCATATGTCAGAGACATACTGTCTTCCTAGTTT

 a Y F L I H S T S I A A L V V T R K D A K -
 b T S Y I Q O V * Q L L * Q E R M Q N -
 c L F N T F N K Y S S S C S D K K G C K T -

 181 CATGGAAATCTGGCTGAATGCCCTCATGACTATTCAAAGTGTGAAAAAACATTAG 240
 181 GTAACTTTAGCCGACTTGTGGAGTAACGTATAAGGTTTCAACGTTTTGTAAATC

 a H C N L A R N R L H C L F Q S C K N N * -
 b I E I W L E I A F I D Y S S V A K T I R -
 c L T G S G S K S P S T I P K L Q K Q L E -

 241 AGTTCTACTCTGGATGCAAATCTTATTAACGATTCTTCTGAGAAAAATTAGTTAA 300
 241 TCAAGATGAAGACCTAGCTTGTAGAAATTTGCTAGAAAGACTCTTTAAATCAAATT

 a S S T S R M Q I F I T I L S C E N * F * -
 b V L L L G C K S L * R F F F L E K I S F K -
 c F Y F S D A N L Y N D S F L R K L V L K -

 301 AAAGCGGAGACAAAGACTAGAAATTGAAACATTACTAATGTTAAATAAAATCAGGTA 360
 301 TTTGGCTCTGTTCTCATTTAACCTTGTAAATGATACAATTATTAGCTTCATT

 a K A E S K E * K L K H Y * C L N K I R * -
 b K R A K S R N C N I T N V * I K S G N -
 c S G E Q R V E I E T L L M F K * N Q G N -

 361 TGAGGATTATCTATTTTAGATCCTTAAAGGAGCATTATGGAGAAAATTACTTAA 420
 361 ACTCTCTAAATAGATAAAAATCTAGTAAGAAATTCTCTGTAAACCTCTTTAAATGAATT

 a C G L F Y F L D H F L R S I M E K I T * -
 b E D Y S I F I T S * G A L W R K L L N -
 c R I I L F F R S L L K E H Y G E N Y L I -

 421 TACTAAAAGGTAAACAGTGGATTATTCCTACCCAAACATGATGAGTATAATTAAAT 480
 421 ATGATTTTCATTTGTCACCAACCTAAAGGATCGGGTTACTACTCATATAATTAA

 a Y * K V N S L D Y F P S Q Q C C V Y * I -
 b T K R * T V W I I S L A N N D E Y I K F -
 c L K G K Q F G L F P * P T M M S I L N S -

FIGURE 12 (cont.)

CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACAAAGACAAACTGCTAT
 481 ----- 540
 GTATACCTCTTACTCACTGTTCCTAGACGTATGTAGTCGAATGGTTCTGTTGAGCGATA

 a b c
 H M R M S Q R I S I H Q T Y Q R Q T R Y -
 I C E C V K G S R Y I R L T K D K L A Y -
 Y E N E S K D L D T S D L P K T N S L -

 AAAAGCGAAAGAAAAAGTTGTATAATCGAACAGCAGAAGAACATTATGCCATTACTATTCG
 541 ----- 600
 TTTTCGCTCTTTTCAAACATTAGCTTGTGCCTCTTGAAATAACGTAATGATAAGC

 a b c
 K T Q E K V C * S N S S R R T Y C I Y Y S -
 K R K K K F D N R T A E E L I A F T I R -
 N A R S K O Q N N L L H L L F V -

 TATGGGTTTATCACATTGTTAGCTATCGAGCGTAACCTCCGAGCTTCTGAGACAAT
 601 ----- 660
 ATACCCAATAATGTAAACAAAATCATAGCTGCCACTTGAGGGCTAGAACACTGTGTA

 a b c
 Y G F Y Y N C F R Y R R C T P E S C D N -
 M G F I T I V L G I D G E L P S L E T I -
 W V L L L O L F * V S T V S R V L R Q L -

 TGAAAAAGCTGTTAACACTGAAGGAATCGCAGCTGAAAGTTCTGATGTGATGCGAT
 661 ----- 720
 ACTTTTTCGACAAATGTTGACTCTCTAGCGTCAGACTTCAGACATACACATACCGTA

 a b c
 C K S C L Q L K E S O F C K F * C V C H -
 E K A V Y V N C R N R S S E S S D V Y A I -
 K K L F T T E G I A V L K V L H C M P L -

 TATTTGTGAATTAACTCAAATATCTTATCTAAATTAAATGGATAGCTATAGAAACAA
 721 ----- 780
 ATAACACCTTAAATAGGATTTAGATAAGTAGTTAAATTACCTTATCGATATCTTGTGTT

 a b c
 Y F V N I S Q I S Y L N L M D S Y R N K -
 I L C E I N L K Y L S I R N E S D V Y A I -
 F C E L I S N I L S Q F N G * L * K Q T -

 CCAAATAAACCATGCAAGTTAAATGGATATACGTTAAATCTTGGGACAAATCGACAC
 781 ----- 840
 GGTATTATGGTAGCTCAAATACCTTATATGCAATTAGAAAACCCGTGTTACGTGTT

 a b c
 P N K P C K F N G I Y V K S F G T N A H -
 Q I N H A S L S M G I E Y T L N P L G Q M H T -
 K * T X Q V L W N I R * I L W D K C T L -

 TGATTTATATGGATCTTAAAGCATAGATACAGAATGCTTACAGACTGATTAGC
 841 ----- 900
 ACTTAAATATAACCTAACGATTCGATCTATGTGCTTACGAAATCTCGACTAAATCG

 a b c
 C I Y I C F L K R E T E C F R D C F S -
 E F T I L D S * S I D T Q N A L E T D L A -
 N L Y W I C K A * I H R H D L * R L I * L -

 TTAACACAGATTCTGCTTACTCTGGCTATCTTATATCTTAAAGAACGCA
 901 ----- 960
 AATGTTGCTAATGGACAAAATCTGAAAGAGACTAGAGAATATAGAAAATTTCTCGT

 a b c
 L Q Q I T C F D Y S C S S L I S L K E A -
 Y N R L P V L I T L A H L L Y L * K K Q -
 T T D L L F C L L L I S Y I F K R S R -

 GGCAGAAATGAAAGAACGACTAAAGAACGAGATTCAAAATTGTTGATCTCTGTAACC
 961 ----- 1020
 CGCGTTTACTTTCTCTGATTCTCTCTAAAGTTTAAACAACTAACAGAACATTG

 a b c
 G E M K R R L K K E I S K F V D S S V T -
 A X C K C E D * R K R F E Q N L L I L L * K K Q -
 R N E K K T K E R D F K I C C F F C N R -

 GGAAATTAACACAAAGAAATTTAGCAACGAAAAAGAACGAGACTATCACAACTCTGATTC
 1021 ----- 1080
 CCTTAATTGTTCTTATATCGTTCTTCTCTCTGATAGTGTAGGACTAAAG

FIGURE 12 (cont.)

T T A A G A T T C A A A A T T C A G G T A A G G A G A T A C A T T C A T T A A A T T C A T A T A T T A T A G 1140
 A A T T T C T A A G T T T T A A G G T C A T T C T C T C T A G T G A A G T A A T T T T A A G T T A A T A T A C
 a b c L K I S K I P G K R D T F I K I H I L * -
 * R F Q K F Q V R E I H S L F I Y Y S -
 K D F K N S R * E R Y I H * N S Y X I V -
 T T T T C A T T C A C A G C T G T A T T T T C T T T A C A A T A T T T T G A T T A C T G G A A 1200
 A A A A G T A A G T T C G A C A A T A A G A A G A T A A G A T A A G T T A A A A A C T A T C G A C C T
 a b c P F I S O L L F S P I L T I F P D * L E -
 F S F H S C L L L S * Q Y F L I S W K -
 F H F T A V I F F Y L N N I F C L A G S -
 G T A A A A G T A T C A A A T A A G A G A G C G C T G A C T G G A G T A A C T T A G C T T A T C A C A T C A T 1260
 1201 C A T T T T C A T G T T A T T C T C T C G A T C T G A C T C C A T T G A A T G A A T A G T O A G T A
 a b c V K S I K * E K R * T E V T * L I H I H * -
 V K V S N K R S A R L R * L S L F T F I -
 K K Y Q I R E A L D C G C N L A Y S H S * -
 A G A T C G A C C T T C A T A T A C C A A T A C G A T G A T A A G G A A C A G C A G T C A T C G T T T T A A A A 1320
 1261 T T C A G C T G A A G T A T A T A G G T A T G T C A T C A T T C C T T G C G T C A G T A G G C A A A A T T T T
 a b c R S T F I Y P I R C * G N S S H P F * K -
 R D P S Y I Q Y R D D K E T A V I R F K N -
 I D L H I S N T M I R K Q Q S V L K I -
 T A T G C T A T G A G G A T A A T T T T G A G T C A G A A G A T G Q G C G G A A N T C T T A A T C A A A A 1380
 1321 A T C A G A T A C T C T G A T T T T T A A A T C G A T G T C T T T A C C T C G G C T T A G A A T T A G T T T T
 a b c * C Y E D * I F R V K K W S R N L N Q K -
 S A M R T K F F L E S R N G A E I L I K K -
 V L C G L N F * S Q E M E P K S . S K R -
 G A A T T G C G T C G A T A T T G C A A A G A T C G A A C T C T A A T C T T C G T T A A A G T A T T A C C A 1440
 1381 C T T A A C G C A G C T A T A A C G T T T T C T G C T G A T T T A G A A G C A A T T A T C T A A T G G T
 a b c E L R R Y C K R I E L * I F R * V L P -
 N C V D I L K N R S N S K S F V N K Y Y Q -
 I A S I L Q K N R T L N L S L I S I T N -
 A T C T G A T T G A T T G A A G A T T G A C G A G G C A A T G C A C A G A A G T C A T T A A G A A T T A A A A 1500
 1441 T A G A A C T A A C T T C T C A A T G C T C T T G A C G T G T C T T C T A G T A A T T T C T T T T T T T T T
 a b c I L I D C R D * R G N C T E D H * R N K -
 S C L I E E I D E A T A Q K I T I K E T I K -
 L D C L K R L T R Q L H R R S L K K * S -
 G T A A C T T T T A A T T A G A A G A T A A A C T A A A T T A C T A A T A T A G A G A T C A C G G A T C T C C A A 1560
 1501 C A T T G A A A A T T A A T T A C T C T C T T G A T T T A A T G C T T A T A T C T C T A G T G C T G A A G T T
 a b c V T F I N * R I N * I T N I E I S D L Q -
 * L L L I R E * T K L L I * R S A I F N -
 N F Y * L E N K L N Y * Y R D Q R S S I -
 T T G A C G A A T A A A A G C T G A A C T A A A A A A A T A C A A C C T T G T C A A A A T 1620
 1561 A A C T G C T T T A T T T C G A C T T G A T T T C A A T C T G T T A T T T T T A T G T T T G G A A C C A G T T T A
 a b c L T K * K L N * S * T I K N T N L G Q N -
 C R N K S C T K V R Q * K I Q T L V K I -
 D E I K A E L K L D N * K Y K P W S K Y -
 A T T G A G G A A G G A A A G A G C A G T G A A A G G A A A A A T A A G G C A A T A A A A A A A T G A 1680
 1621 T A M T C C T T C T T T C T C T G G T C A A T C G T T T C T T T T T A T C C C T T A T T T T T T A C T
 a b c I E E G K E D Q L A K E K I R Q * I K C -
 L R K E K K K T S * Q K K K * G N K * N E -
 C G R K R R P V S K R K N K A I N K M S -

FIGURE 12 (cont.)

1681 GTACAGAACTGAGAAAATAAAGATTTTATTTTCAATTAAATTGTAAAAAGAGGGGTT 1740
CATGCTTCACTTCTTATTTCCTAAATAAAAAAGTTATTAAATAACTTTCTCCCCAA

a V Q K C R N K R F I F F N N L L K R G V -
b Y R S E E I K D L F F S I I Y C K E G F -
c T E V K K * K I Y F F Q * F I E K R G F -

1741 TTGGGGTTTGGGGTTTGGGG 1762
AACCCTAAACCCCTAAACCC

a L G F W G F G -
b W G F G V L G -
c G V L G F W -

FIGURE 13

2	EVDVNDQANQHNGIHSALKTCEEIKAKTLYSWIQVNRVCRNQSQSHYKDL	51
19	ELELEMQENQNDIQVRVK...IDDPKQY..LNVNTAACLLQEGSYYODI	62
52	EDIKIFQAOTNIVATPRDYNEEEDFKVIARKEVF..STGLMELIDLKCLVELL	100
63	DERRYIIKATT...EVAESDEFICQALVQVIRNEYIRETTTYVIF...	107
101	SSSDVSDSRKOLQCQFCGFGKQNLGNALAKTHILPLASTQKOVYFDDNQYRUM	107
	...CVHMKNTOPPIFQYKPNKAVLNUPLDCEFAQVLYI	144
151	IGNELFRHLYTKYLIPORTSEGTLVQFCGNNGVFDHLKVNWDKFDKOKGGA	200
145	DFDATEFKNLY.....DLRILSODIRKELTFPKKLCLRQCVRSKE	181
201	ADMNE...PRCCSTCKYVNVNEKDHFHNINNVPNRNNMSRSRTIFYCTHE	247
182	SEFNEYQLOQCYTES..QRKXITMFYLSVTNQKWDQTHKK...	220
248	NNRNOFFKKHEFSVNNNNISAMDRQQTIFTNIFPRRNRIIRKKLKDVKIEKI	297
221	.RKENILTLKLQAIKESEDKSKRETG...DIMHNMEDAAKPLPAVMKKI	264
298	AYMLEVKDGFNFNNYYLTKSCPLPENWRERKKQKIEINLINTREEKSKYYEE	347
265	AKRQHNA...KHMKAFKIPINSTLESKYLTPKD	294
348	LFSYTTONKCVTFQIMEFFNYILPKDPLFDTNRRNFKOFVKVXVLYENLKH	348
295	LIFKCHISPE...KERVYKILKGKYPKTEEEYKAAFGDOSASAPEN..PE	338
398	LIHKNNLLEKINTREISWMQVETSAKHFYYFDHENEIYVLUWKLLRWIFEDL	447
339	LAGKRHKIEISKWTWENELSAGKNTAEWVNDSLISNOLPYAMHLRLNSL..	386
448	VVSLRCFFYVTEQQKSYSKTYYYRKNINWDVINKMSIAIDLKKETLAEVQE	497
387	...ILKAGVSD...	394
498	KEVEEWKKSLGFAPGKLRLIPKTTFFRIPMTFNKKIVNSDRKTTLTTNT	547
395	...TTHS	398
548	KLLNASHMLKTLKXRMFKDPPGFVNPYVNDVVKKYEEFVCKHKVOKCOPKL	547
451	IVINK...	415
598	FFTADMEICKYDSVNRKELSTFLKTTKLSSDFWIMTAOILKRNKNIVID	647
416	F..PLQPFSAIEAVN.EAVTKGFFAKK...RENNMLKGIEAVKE..VUJ	457
648	SKNFKPKKMDYFRQKFQKIALEGQYPTLFSVLENEQNLLNAAKNTLIVE	697
458	KTDEEKDM...ELEQTEEGFVKVNEGIGKQYINSIELAIK	496
698	AQKRNYYFKDKNLLOPVINOCYNNINFNGKFKYKOTKGIPQGLCVSSILSS	747
497	IAVNKNLDEIKGHTAIFSDVSGSMSTSMSGACKYGSVRTCLECALVGL	546
748	FYATLEESSLGFLRDESMNPENPNVNNLWRLTDYLLTTQENNANVLFI	797
547	MVKORCEKSKYTFISSLPSQPCNCXLYEVL...	576
798	EKLINVSRENGFKFNNMKK.LOTSPLSPSKPAKYGMDSVEEQNIVODYCD	846
577	PDEELRPSHQKLLQEGKLGCG...TOPFYECIDEWTKNKTHVD	617
847	WIGISIDMKTLALMPNNIHLIREGILCTLNUNLHOTKKSASWLKKKLKSFLM	896
618	NIVILSDMMIAEYGSDINVRGSSIVNSI...	653
897	NNITHYFRKTITTEDFANKTLNKLPISSGGYKYMOCAKEYKD.HFKKNLAM	945
654	PNIKIF...AVDLEGY...KCLNLGDEFNNENNYKIKFGM	687
946	SSMIDLEVSKIIISVTRAFFKYLVCNICKOTIPGEHEHYPDFLSTLKHFIE	995
688	SDSI...LKFISAKQGGA...	NHVE
996	IESTKYYIPRNVC 1008	
707	VI...KNAFAOKIG 712	

FIGURE 14

132 LSTOKQYFFQDEWNVRAMIGNEL. FRHLYTKYLIFQRTSE.. GTUVQFC 178
1 HSRRNQ. KRPQAPINETNLDFVLQNLEVYSQIEHYKTQQQI 43
179 GNNVFEDHLXVNDKFQKKGAAQNEPRCCSTCKVNKEKDHFLLNN 228
44 KEEDLKLKKFNNQDDGQNSCNDDEE. NNSNKQELLRRV 84
229 VPNNNNMSRTRIFYCTHFNRRNQFFXHEFVSNKANNISANDRAQTIFT 278
85 QIKQQVQLIKK. VGSKVEKDMLNLNEDENK 114
279 IFRNRNIRKKLKDVKIEKIAYHLEKVKDFNFNYYLTKSCPLPENWRERKQ 328
115 GLSEQQVKEEQLRTTIEOEVKYOLVFNNDYGLDNLNESGCHRRHRETDY 164
329 KIENLINKTREEKSKEYEEFLSYTTDNKCVTQFINE. FFYNILPKPDFLTG 377
165 DTEKWFIEISHDQK. NTVSITYANQKTSYCWWLKOYFNK 200
378 RNRNFQKVKVYVELNKHELTKNNLLEKINTREISWMQVETSAKHYY 427
201 NYDHLNVSINRL. TEAEFYAFDDFSOTIKLTNSYQTVNID. 242
428 FDHENIYVLMKLLRM. FEDLUVSLIRCCFFYVTEQOKSYSKTYYRKN 475
243 VNFDNNCLCILALLRPLLSSLERPNILNIRSYY. TRQYQNFKEKIGELLETI 290
476 WDVIKKMSIADLKKETLAEEQKEKEVEEWKKS. LGFAPGKLRLLPKKTTFRP 525
291 FAVVFSHR.LHOGIHLQVPCEAFQYLVNSSS0ISVKDSOLQ 330
526 IMTFNKKIVNSDRKTTKLTTNTKLLNSHMLKTLKNRMFKDPFGFAVNY 575
331 VYSFSTDLLKVL. TNKVDQYDKFLQFPRLTHVSQAIPTSATNAVEN 378
576 DDVKKYEEFVCWKWQVQCPKLF. FATMDIEKCYDS.. VNREI 615
379 MVLLKKVHH. ANLNLVSPQTFNPDPYFVNQHUKLEFGLPEPNILTHQK 426
616 LSTFL. KTKLSSLDSDFWIMTAQILKRRNNI. .VIDSKNFRKKEMK 657
427 LENLSSIKOSKLNKFLRNPYTTVVAQETSRKQILQKATTIKHLKNNNNQ 476
658 DYFRQKFQKIALEGQQYPTLFSVLEN. QNDLNAKKTLLIVEAKQRNYFK 705
477 EETPETKDETSESTSGWKFHDHLSLTLEDPSVN. LQATOEIY 520
706 KDNHLLQPVINIQCYNYINFNGKFKYQTKGIPQGLCVSSILSSFYATLEE 755
521 DSHKLLIRSTNLKHKFKLSSYKVEHEKSMNDTFLDLKNI. YETLNN 564
756 SSGCFURDESHPENPVNVNLMRLLTDYLLITTOENNAVLIEKLINVS 805
565 LKRCSVNISNPNGHNSNISYELTN. KDTSTYFKFLTLNQE 600
806 ENOFKFNKKLQTPSLPSKPKAYGHDSVEEONIVQDYCDWIGISIDMK 855
601 LOHAKYTFK. ONEFOPNNVNSKAKIESSSLESLEDIDSILCKSIAASKNLQ 648
856 TLAJMPNINRIZEGICLCTLNLMOT. KKASMWLKK. KLSPLMNNITH 901
649 NVNI. IASLVPNNIQKPNPKNVLFLKFQFQQLKNLENVSINC 691
902 YFRKTI. TTEDFANKTTLKLFISCGGYKYNQCAKEYKDNFKKNLAMSSH 948
692 ILDQHILNSISEFLEKNNKIKAFILKRYLLQYLDYTKLFTLQLQPL 741
949 IDLEVKSKIIYKVT. RAFFKYLVCNPKD. IFGEEHY 982
742 NOVYINQOLELTVSEWHQVWENHKQKAFYEPLECEFPIKESSTOTLQLIDF 791
983 PDFFLS. TLKHFIEIFSTK. IFNRVCMILKAKEAKLKSDOCQSLIQ 1028
792 DQNTVSDDSIKRILESESSESYHHYLRLNPSQSSSLIKSENNEEIQELK 840

FIGURE 15

4 DIDLDDEIINLLPNTFKYSSCSKDKGCKTLKGSKPSLTIKP..... 47
617 NVKSAKIESLSSLESLEIDSLCKSIAASCNQNVLNIIASLLYLPNNIQKNP 666
48LOQQLQEFYFSANLYNDSFLRKLGVLVLSGEQRVE.....IETLLM 86
667 FNKPNNLFFKFQEPLKNLNENVSINCILDQHILNSIEFLEKNNKKIAFIL 716

FIGURE 16

1 MEMIDIDLDIENL.....LPNTFNKYSSSCSDKKGCKTLKSGSKSPS... 42
491 IELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLEC 540
43 LTIPIPKLOKQ.....LEFYFSDANLYNDSFLRKLVLKSGEORVEIETLL 85
541 ADVLGLHVKQRCEKSSFYIFSSPSSQCNKCYL.EVDLPGDELRPSMQKLL 589

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FIGURE 17

FIGURE 18

telomerase p43 LQKQIEFYFSDANLYNDSEFLRKLVLKSGEQRVEIETLLM
human La ICHQDEMYFGDFNLPLPKDFKLKEQI.KLDEGWVPLEIMIK
Xenopus LaA ICEQIEVYFGDFHLPLPRDKFLKQQI.LLDDGWWVPLETMIK
Drosophila La ILRQMEVYFGDANLNFRDKFLREQIGKNEGDGWVPLSVLVT
S. c. Lhp1p CLKQMEFYSEEFNFPYDRELRTTAEK.NDGWVPISTIAT

FIGURE 19

FIGURE 20

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL
VNVTAAACLQEGSYYQDKDERRYIITKALLEVAESDPFICQLAVYIRNELYIRTTIN
YIVAFCVVHKNTQPFIKEYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS
QDIRKELTFRKCLQRCSVRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTQ
KKRKENILLLQAIKESEDKSKRKGDIMNVEDAIKALKPAVMKKIAKRQNAMKKHMK
APKIPNSTLESKYLTFKDLIKFCHESEPKERVYKILGKKYPKTEEEYKAAGFDSASAP
FNPELAGKRMKIEISKWTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGV
SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFAKKRENMNLLKGQIE
AVKEVVVEKTDEEKKDMELEQTEEgefVKVNEGIGKQYINSIELAIKIAVNKNLDEIKG
HTAIFSDVSGSMSSTSMSGGAKKYGSVRTCLECALVGLMVQRCEKSSFYIFSSPSSQ
CNKCYLEVDLPGDELPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKHVDNIVILSD
MMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFAVIDLEGYGKCLNLGDEFNENNYI
KIFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK

FIGURE 21

FIGURE 22

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQIK
EEDLKLLKFKNQDQDGNSGNDDDEENNSNKQQELLRRVNQIKQQVQLIKVGSKVEK
DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMHDYQLDLNESGGHRRHRR
ETDYDTEKWFEISHDKNYVSIIANQKTSYCWLLKDYNKNNYDHLNVSINRLETEAE
FYAFDDFSQTIKLTNNSYQTVNIDVNFDNNLCILALLRFLLSLERFNILNIRSSYTRN
QYNFEKIGELLETIFAVVFSRHLQGQIHLQVPCAFQYLVNSSSQISVKDSQLQVYSF
STDLKLVDTNKVQDYFKFLQEFPRLLTHVSQQAIPVSATNAVENLNVLKKVKHANLNL
VSIPTQFNPDFYFVNLQHLKLEFGLEPNILTQKQLENLLSIKQSKNLKFLRLNFYTY
VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED
FSVNLQATQEYDSLHKLLRSTNLKKFKLSYKEMEKSMDTFIDLKNIYETLNNLK
RCNVNISNPNGNISYELTNKDDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSAKIE
SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNNLFFKQFEQLK
NLENVSINCILDQHILNSISEFLEKNKKIKAFLKRYYLLQYYLDYTKLFKTLQQLPE
LNQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSLQQLIDFDQNTVSD
DSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP
LCLPTGTYYDYNNSDRW

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FIGURE 23

MKILFEFIQDKLDIDLQTNSTYKENLKGCGHFNGLDEILTTCFAL
PNSRKIALPCLPGDLSHKAVIDHCITYLLTGELYNNVLTFGYKIARNEDVNNSLFCHS
ANVNVTLLKGAAWMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK
WVQRSSSSATAAQIKQLTEPVTNKQFLHKLNIINSSSFPPYSKILPSSSSIKKLTDLR
EAIPTNLVKIPQLKVRNLTQKLLKRHKRLNYVSILNSICPPLEGTVLDLSHLSR
QSPKERVLKIIIVILQKLLPQEMFGSKKNKGKIIKNLNLLSLPLNGYLPDFDSLKKL
RLKDFRWLFISDIWFTKHNFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVTI
VYFRHDTWNKLITPFIVEYFKTYLVENNCRNHNSYTLSNFNHSKMRIPKKSNNER
IIAPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE
FKQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN
TNTGVLKLFNVNVNASRVPKPYELYIDNVRTVHLSNQDVINVVEIFKTALWVEDKCY
IREDGLFQGSSLsapIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV
INIKKLMAGGFQKYNANKANRDKLAVSSQSDDDTVIQFCAMHIFVKELEVWKSSTMN
NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF
KDLSINVQTQNMQFHSFLQRIIEMTVSGCPITKCDPLIEYEVRFITLNGFLESLSSNTS
KFKDNIILLRKEIQHLQAYIYIYIHVN

FIGURE 24

Oxytricha
Euplotes

LCVSYILSSFYANLEENALQFLRKESMDPEKPETNLLMRLT
LCVSSILSSFYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIGURE 25

FIGURE 26

ATTTATACTCATGAAAATCTTATT CGAGTCATTCAAGACAAGCTTGACATTGATCTACA
GACCAACAGTACTTACAAGAAAATTAAAATGGGTCACTTCAGAAAAATAGCATTACCATGCCTTCCTGG
TGACTTAAGGCAAAAGCAGTCATTGATCACTGATCATTACCTGTTGACGGCGAATT
ATACAACAAACGCTACTAACATTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAAATAG
TCTTTTTGCCATTCTGCAAATGTTAACGTTACGGTACTGAAAGGCCGTGCTTGAAAAT
GTTCCACAGTTGGTCGGTACATCGCATTGTTGATTATGATCAATTATAACAGTAAT
TCAATTAACTGGCAGTTTCTCAAACTGTTGGAACAGATGTAACGAACTCTCATCT
GCCGCCAAATGGGTCACGATCATCCTCATCATCCGAACTGCTGCCAAATCAAACA
ACTTACAGAACAGTGACAAATATAACAACTTACACAAGCTCAATATAATTCTCTTC
TTTTTTCTTATAGCAAGATCCTCTTCATCATCATCTCAAAGCTAATGACTGAC
GAGAGAACGTTTTCCACAAATTGGTAAATTCCCTCAGAGACTAAAGGATCGAAAT
TAATTGACGCTGCAAAGCTTAAAGAGACATAAGCCTTGGAAATTACGTTCTATT
GAATAGTATTGGCCACCATGGAAAGGAGCCATTGGACTTGTGCGATTGAGTAGGCA
ATCACCAAAGGAACGAGCTTGAATTATCATTGTTATTACAGAAAGTTACCCCA
AGAAATGTTGGCTCAAAGGAAAATTAAAGGAAAATTATCAGAAATCTAAATCTTATT
AAGTTACCCCTTAACTGGCTATTACCATTTGATAGTTGTTGAAAAGTTAAGATAAA
GGATTTCGGTGGTTCTTGTATTTGGTCAACAGCACAATTGGAAAACCTT
GAATCAATTGGCGATTGTTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTT
ACAGACTTTTACTGCACCGAAATATCTCTACAGTGACAATTGTTACTTAGACA
TGATCTGGAAATAACTTACCCCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTT
CGAAAAACAGCTGTGAAAGACCATTAAGTTACAGCTGGTCAATTCAATCATAGCAA
AATGAGGATTATAACCAAAAAAGTAAATAATGAGTTAGGATTATTGCCATCCATGCG
AGGGGAGAGAACGAGAAATCACAATTATAAGGAGAAATCACAAAATGCTTACAGCC
CACTCAAAATTGGATAATCTAACGAAACAAAAGGCCGACTAGTTTACTAAATATA
TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTAAAGCAGAGACTTTAAAGAAATT
TAATACTGGCTTACAGAGCTTTCTGATGAAATTGATGTCACATCTGCTGATGTC
CATACAAAGGGATGGAATGAGGATACTAACGGATGCGCTTAAAGAATGGGTT
TTCTGTTAGATCTCAATATTCTCAATACCAATACAGGTTATTGAAGTTATTAAATGT
TGTTAACGCTAGCAGACTACAAACCTTATGAGCTTACATAGATAATGTGAGGACGGT
TCATTTCATCAATCAGGATGTTATAACAGCTTGTGAGATGAAATTAAACAGCTT
GTGGGTGAAGATAAGTGTACATTAGAGAAGATGGTCTTTTCAGGGCTCTAGTTTATC
TGCTCGATCGTGTATTGGTGTATGACGATCTTCTGGAGTTTATAGCGAGTTAAAGC
CAGTCTAGCAGGACACATTAAATTAAAATCTGGCTGAGCTTCTTATAATATCAC
AGACCAACAGAAGTGATCAATATCAAAGCTGGCATGGGGGATTCAAATATCAA
TGCAGAAGCCAAATAGAGACAAAATTAGCCGTAGCTCCAACTCAGATGATGACGGT
TATTCAATTGGTCAATGCACATATTGTTAAAGAATTGGAAATTGGAAACATTCAG
CACAATGAATAATTCCATATCCGTTGAAATCTAGTAAAGGGATATTTCGAAGTTAAT
AGCGCTGTTAAACTAGAAATCTTATAAAACATTGACACAAATTAAATCAACAAA
CACCTTCTCATGCAAATTGATCATGTTGAAAGAACATTTGGAATCTTATAAAATCTGC
TTTAAGGATCTACATTAAATGTTACGCCAAAATGCAATTTCATTGCTTCTAACACG
CATCATGAAATGACAGTCAGCGGTTGTCACATTAGCAATTGATCCTTATCGAGTA
TGAGGTACGATTACACATATTGAATGAGGATTGGAAAGGCCATCTCAAACACATCAA
ATTAAAGATAATATCATTCTTTGAGAAAGGAAATTCAACACTTGCAAGC

FIGURE 27

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR
AERLTSRVKALFSVLNYERA

FIGURE 28

GCCAAGTCTCTGCACTGGCTGATGAGTGTACGTCGAGCTGCTCAGGTC
TTCTTTATGTCACGGAGAACCGACTTCAAAGAACAGGCTTCTTCTAC
GGAAGAGTGTCTGGAGCAAGTGCAGGAACTGGATCATGAGCAGACTTGA
GAGGGTGCAGCTCGGGGACGTTGTCGGAAGCAGAGGTCAGGCAGCATGGG
AGCCAGGGCCGCCCTGTCAGTCCAGACTCCGTTCATCCCCAAGCTGACG
GGCTGGCCCGATTGTGAACATGGACTACGTCGAGGCCAGAACGTTCCG
CAGAGAAAAGAGGGCCGAGCTCACCTCGAGGGTAAGGCAGTGTTCAGC
GTGCTCAACTACGAGCGGGCGCG

FIGURE 29

MTEHHTPKSRLRFLENQYVYLCTLNDYQLVLRGSPASSYSNICERLSDVQTFSIFLHSTVVGF
DSKPDEGVQFSSPKCSQSELIANVKQMFDESERRNLMLKGFSMNHEFRAMHVNGVQNDLV
STFPNYLISILESKNWOLLEIIGSDAMHYLLSKGSIFEALPNNDNYLQISGIPLFKNNVFEETVSKKRK
RTIETSITQNKSARKEWSNSISISRSFISYRSSYKKFKQDLYFNLHSICDRNTVHMLWLQWIFPRQFG
LINAQVKQHLHKVPLVSQSTVVPKRLKVKYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS
YSLKPQNQVFAFLRSILVRVFPLIWNQNQRIPEIILKDETFKLRLSRYESFSLHYLMSNIKISEIEWLVL
GKRSNAKMCLSDFEKRKQIFAEFIVWLYNFSIIPILQSFFYITTESSDLRNRTVYFRKDIIWKLLCRPFIT
SMKMEAEEKINENNVRMDTQKTTLPPAVIRLLPKKNTFRJITNLRKRFLIKMGSNKMLVSTNQT
LRPVASILLKHLNEESSGIPFNLEVYMKLLTFKDDLLKHMGRKYYFVRIDIKSCYDRIKQDLMFR
IVKKKKLDPEFVIRKYATIHATSDRATKNFVEAASFYFDMVVFPEKVVQOLLSMKTSDTLFVDFVDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVVDDFLFITVNKKDAKKFLNLSLRGFKEKFNFSTSLEKTVINFENSNGIINNTFFNESKKRMPPFG
FSVNMRSLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFDITHNSKFNSCCNI
YRLGYSMCMRAQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFC
LGMRDGLKPSKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLFHRRIA

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FIGURE 30

FIGURE 30 (cont.)

A T C G t a c g i g i c g g i c t c g a g a c i t c a g c a a t a t g a c a c a t c a g G C T T T T T T G C T C T G G A A T G A G A G A T G G T T G A A A C C C T C T T
T C A A A T A T C A T C C A T G C T C G A A C A G G T A A T A T A C C A A T T C A G T C A T T G A C T G A T C T T A T C A A G G C G C
T A A G A C C A G T T T G C G A C A G G T G T T A T T T A C A T A G A A G A A T A G C T G A T T A A T G A T T A T C A C T C E T
t a t t a c t g g t g t c t t a a c a a t t a t t a c t a g t a t a g c t g a c c c c a a a g c a a g c a a g c a a t a c t a g t a t t c t a g t a a g t a a a a t t a t c t c g t t a t a g t t g a l t g a c t t g i c t t
a t c c t t a t a c t t t t a a g a a a g a g t t g a c a g t i g g t g c i g a c t a c t g c c c a c a t g c c c a t t a a a c g g g a t t g g t t a a a c a t t a a a g t a a t a c a t g a g g c t a a t c t c t t c a t t a g
a a t a a g g a a g t t g g t t t a t a a t g a a t a a t g c c c c a c t a g c a a a a g c a a g a g a t t a t c t c t a a a c a a g g g g a t t a g a g c a t a t c c g a a g g g a a a a g a g a g a t t a t
a c c c a g t t g t g a a g a a g c a a g g a t t t g a a c a a g c t t c g c a g t a g c a c g g c t a a a t t t g g t g a c c g a a t t t g g t a a a g c c c c a g g f t a t c a t g g t g c c
g c c t i g c t a c i g a g c g a a a a g a a a c t a g g g a t t t g a a t a c t a t a g c t c a t t a a t g c t t a t a a g g t t t t t c c i g a c t c a t t t g c a t g g g t g a a a a g a a a t a
g t g t a a g c c a t t a t g g a t t c c g a a a t a g c c a a t t t c t g g t c t c a a a g c g g a a g t t a a a g a a c t t a t g a a g c t t a g g e t t c a a a a a c t c c t c t g a t t a a a g g g a
g a a t t c t c a c c g a g t g a g g a a t t g g a t t c t a g c t c g t g a g g a a g c c t a a t t t t g c a a a a a a g a a a a t a t c a t g g g a a g a c a t t c t g a l t g a a t c a g a t g c g g a
g a g t a i c t c a c g c g a t c t f g a t t c a a t t c t t t c t g a a t t g t a t g g i c c t a c t g c t c g a c t t c t c g t a g c t a c g c a g t a a g t g a c c a a g g i a c c

FIGURE 31

EST2 pep	FFYCTEISST VPIIVYFRHDT WN---KLIT P-----FIVE YFK-TYLVEN	40
Euploites pep	FFVYTEQQKS YSKIVYYRRK IWDVI-MKMS IAD---LKK ETIA--EVQE	43
Trans of tetrahymen	-----KHKRE GQSQIFYYRRK IMLVLSVKITI VKVRIQSF NKQMKNNNFYQ	44
Consensus	FFY.TE..K. .S..YYRK. IW...-KL.-F..KV..	50
EST2 pep	NVCRMHNNSY- ----- TLSNPNHNSK DPKLPEEKNSNNE EPRDIPRCRG	75
Euploites pep	KEVEEWKPKSL ----- GFAPGKQD FPAKNT- PRKEMTFNKK	76
Trans of tetrahymen	KIQLEENLENLE KVEEKLIPEID SFQKYPPQCKD EPRKEMTFNKK-----	92
Consensus	K...E..... P...GK...P...K...D...E...P...R...KEMTF.RK	100
EST2 pep	ADEEEFTIYK ENHKNAIQPDK QKILEMVRN RPTTSFTKIYS PQTIAADRKE	129
Euploites pep	IVNSDRKTIK LITINIKLILNSHLMLKTKN-----RMEK -DPGEFAVN	120
Trans of tetrahymen	DKQKNIK--- LNLNQILMDS GLVFRKND-----ML-G -QKIGSVFD	13C
ConsensusK..K LN.N..L..S..QL.L..EKN----- ..IG..VF.	150
EST2 pep	FKQRLLKAFN NVL----- EPRDFMFKFD VKSCYD	157
Euploites pep	YD-DVMMEYE EFVCKWQKVQG QPQFQFAIMD IECYCD	155
Trans of tetrahymen	NK-QISEPFA EKPFKWWKNG HSDIYVTL-----	156
Consensus	.K...-R.E. .F..KWK..G E...F..T.D ...CYD	160

FIGURE 32

S-1: FFY VTE TTF QKN RLF FYR KSV WSK
S-2: RQH LKR VQL RDV SEA EVR QHR EA
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DV^S
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

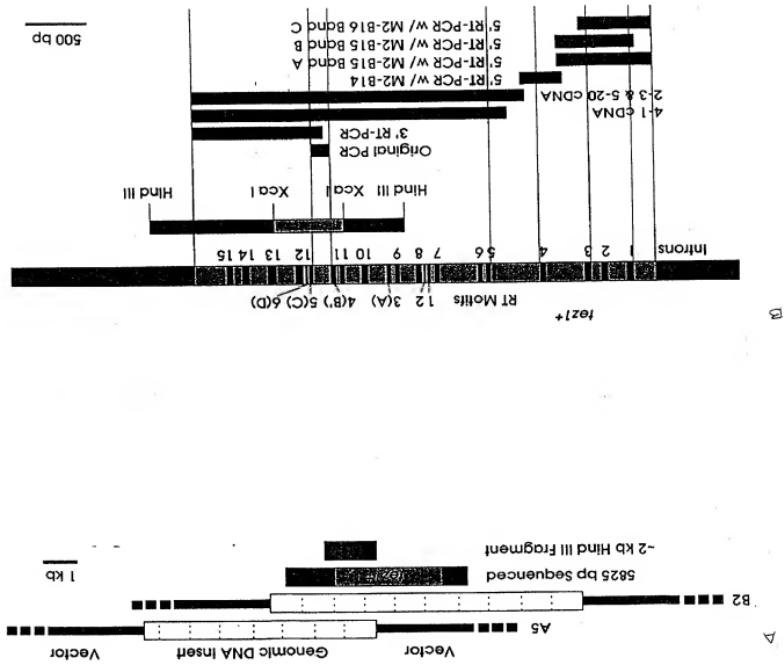


FIGURE 33

FIGURE 34

Poly 4

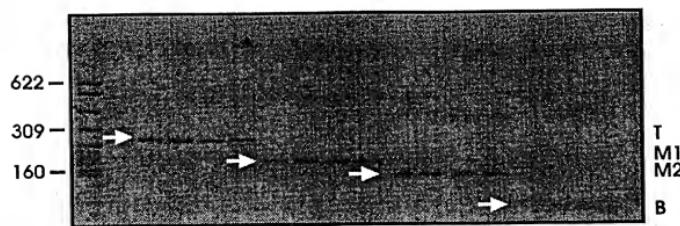
5'- t a a g c c t c g
cag acc aaa gga att cca taa gg -3'
Q T K G I P Q G

4 (B')

5 (C')

3'- D D Y L L I T
ctg ctg atg gag gag tag tgg -5'
a a a a a a a a
t t t t
c c
Poly 1

FIGURE 35



Motif B' (4)
QTKGIPQG

Motif C (5)
DDYLLIT

FIGURE 36

**PCR Product M2 showed Reasonable Match
with Other Telomerase Proteins**

Ot LCVSYILSSFYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123 KGIPQGLCVSILSSFYATLEESSLGLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2 SILSFLCHFYMEDLIDEYLSTKKK-----GSVLLRVV
Sc_p103 DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS
* * * * * * *

Q K V G I P Q G
Caa aaa gtt ggt atc cct cag gg..... <---Actual Genomic Sequence.

Poly 4

t t c
a a g c c tcg
cag acc aaa gga att cca taa gg ---->

Ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

K G I P S G S I L S S F L C H F Y M

GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC CCT AGT CAC AAC AAT GCT

E D L I D E Y L S F T K K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg

V V D D Y L L I T

<---- ctg ctg atg gag gag tag tgg
a a a a a a a
t t t t t
c c

Poly 1

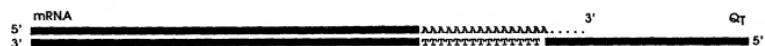
....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence.
D D F L F I T

FIGURE 37

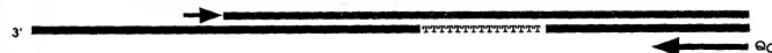
3' RT PCR Strategy



1. Synthesis of cDNA with Q_I Primer.



2. First Round PCR Using Outside Primer and Q_O Primer.



3. Second Round PCR Using Inside Primer and Q_I Primer.



4. Sequence Second Round PCR Products Using Inside Primer or Q_I Primer.

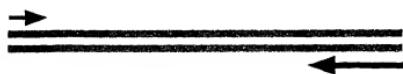


FIGURE 38

A

-Size Selected Libraries from *P. Nurese*

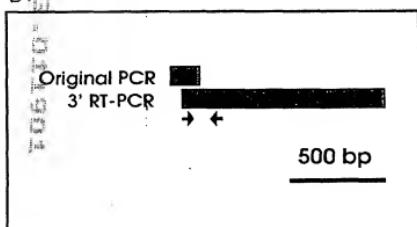
- 3 ~ 4 kb
- 5 ~ 6 kb
- 7 ~ 8 kb
- 11 ~ 12 kb

-Libraries from J.A. Wise
Sau 3a Partial Digest
Hind III Partial Digest

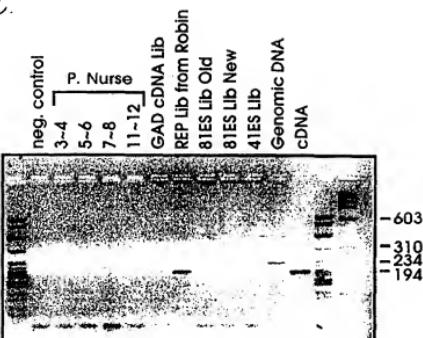
cDNA Libraries

- GAD (Gal Activation Domain) Library
- REP Library from R. Allshire
- REP81ES Library (old)
- REP81ES Library (new)
- REP41ES Library

B



C



D

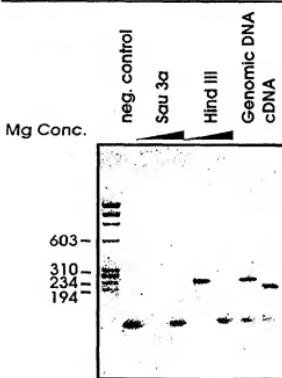
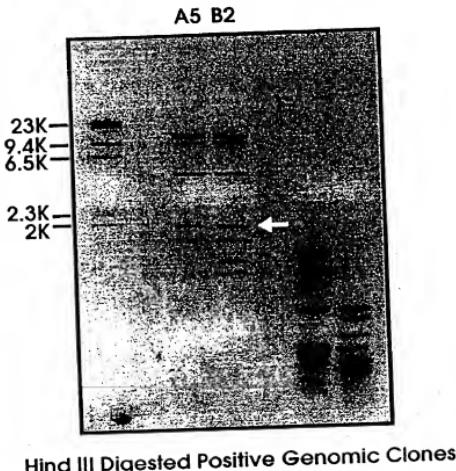


FIGURE 39



TIFF TO EPS2000/600

FIGURE 40

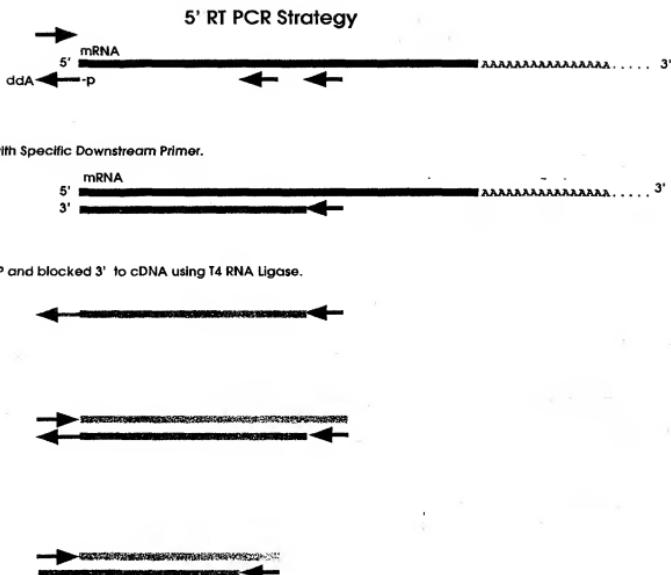


FIGURE 41

Alignment of RT Domains from Telomerase Catalytic Subunits.

S.p. Tez1p	(429).	WLYNSFIIPILQMSFFYITESSDLRNRTVYFRKDIW	... (35) ...
S.c. Est2p	(366).	WLFRLQLIPKIIQTFYCTEISSTVT-IVYFRHDTW	... (35) ...
E.a. p123	(441).	WIFEDLVSVLIRCCFFYVTEQQKSYSKTYYYRKNIW	... (35) ...
	*	*****	*****
	Motif 1	Motif 2	K
p	hh	h K	R
S.p. Tez1p	AVIRLLPKK--NTFRLITN-LRKRF	... (61) ...	
S.c. Est2p	SKMRLIPKKSNNEFRIIAIPCRGAD	... (62) ...	
E.a. p123	GKLRLIPKK--TTFRPIMTFNKKIV	... (61) ...	
	*	***	*
	Motif 3(A) AF		
	h DhD GY h		
S.p. Tez1p	KKYFVRIDIKSCYDRIKQDLMFRIVK	... (89) ...	
S.c. Est2p	ELYMFKFDVKSCYDSIPRMECMRLK	... (75) ...	
E.a. p123	KLFFATMDIEKCYDSVNREKLSTFLK	... (107) ...	
	*	***	*
	Motif 4(B')		
	hpQG pP hh h		
S.p. Tez1p	YLQKVGIQPGSILSSFLCHFYMEDDLIEDEYLSF	... (6) ...	
S.c. Est2p	YIREDGLFPGQSSLASAPIVDLVYDDLLEFYSEF	... (8) ...	
E.a. p123	YKQTKGIPQGLCVSSILSSFYYATLEESSSLGF	... (14) ...	
	*	***	*
	Y Motif 5(C)	Motif 6(D)	
	h F Dhhh	Gh cK h	
S.p. Tez1p	VLLRVVDDFLFIVTNKKDAKKFLNLNSLRGFEKHNKFSTSLEKTVINFENS	. (205)	
S.c. Est2p	LILKLADDFLIISTDQQQVINVNIKKLAMGGFQKYNAKANRDKILAVSSQS	. (173)	
E.a. p123	LLMRLTDDYLLITQZENNAVLFIEKLINIVSRENGFKFMKMLQLTSFPLS	. (209)	
	***	*	*

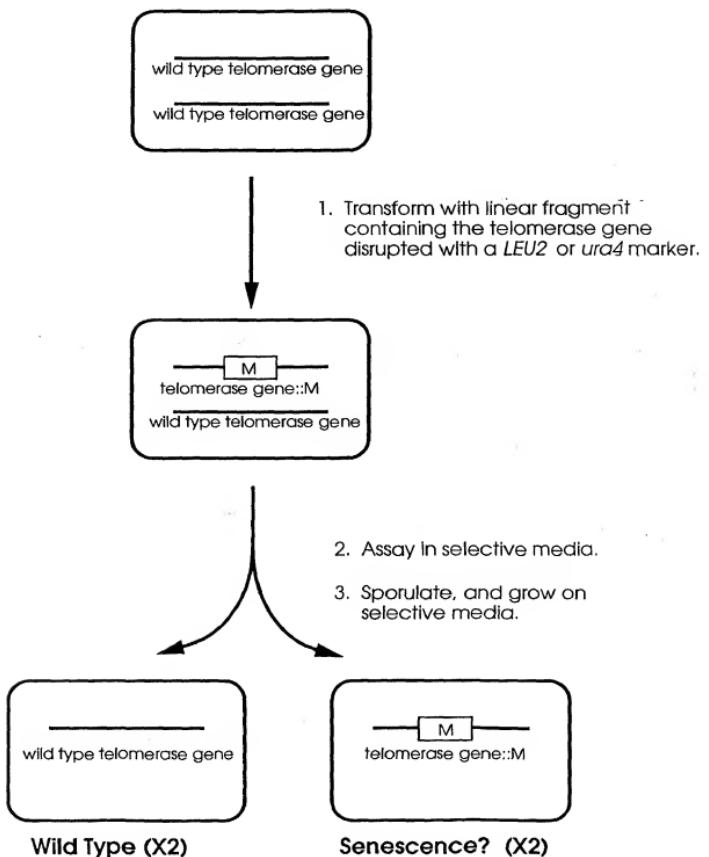
FIGURE 42

A

6

FIGURE 43

Disruption strategy for the putative telomerase genes.



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIGURE 44

An Example of Confirmation of *tez1* disruption By PCR

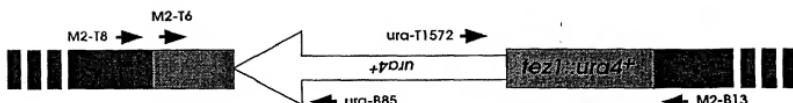
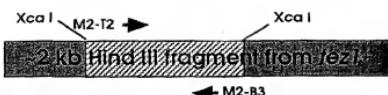
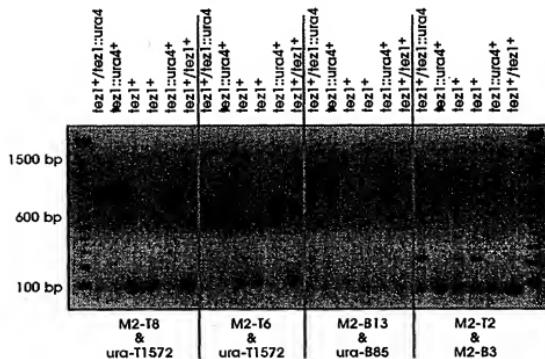


FIGURE 45

Tez1 disruption causes progressive shortening of telomeres in *S. pombe*

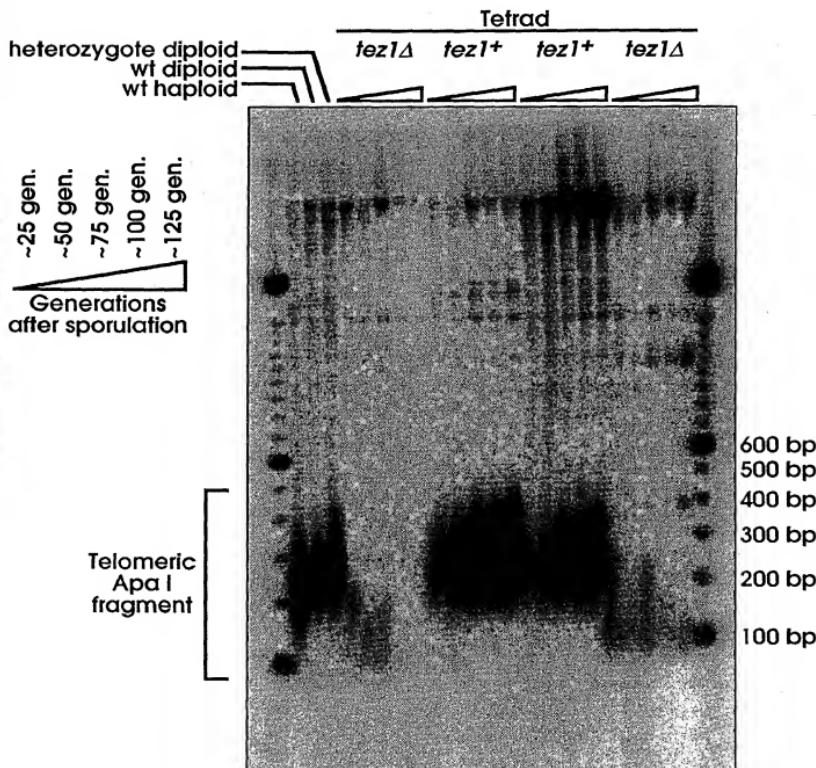


FIGURE 46

1 ggtaccgattttacttcccttcataagctaattgtttcgcgaacgctccaaatctcgaaatatttacaaga 80
81 actcaataacaatccaagtc当地atgggttatagtgatcgataatattctatccatcgatcgta 160
161 ccaagtataaggaaaaaaaagacaacttccccc当地aaagactttactttatatttccaaatataatttcg 240
241 gttcgcttactttaatcggttagctgtacttctagccaaccgcgttctacccgc当地atggat 320
321 agcttgc当地atggatc当地atccatcgatgagactatatttagatttattacatcgatcgat 400
401 ttaacatggaggcttactttatggatgatcgatcgatgttgc当地atccaaacgttgc当地tggaaaag 480
481 gttgataatatttgc当地atccatcgatgttgc当地atccatcgatgttgc当地atccatcgat 560
561 atttagatattcaaaaatttctatccatcaactctt当地atccatcgatgttgc当地atccatcgatgtt 640
641 ccaatataatgtatcatctgtataggctt当地atccatcgatgttgc当地atccatcgatgtt 720
721 ataatctaaatattgttgc当地atccatcgatgtatggatgatgtatggatgatgttgc当地atccatcgatgtt 800
801 gatacttgc当地atccatcgatgttgc当地atccatcgatgttgc当地atccatcgatgtt 880
881 actattttataaaacgtt当地atccatcgatgttgc当地atccatcgatgttgc当地atccatcgatgtt 958

959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018
1 M T E H H T P K S R I L R F L E N Q Y V 20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078
21 Y L C T L N D Y V Q L V L R G S P A S S 40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA AC G TCC TTT TCT ATT TTT CTT 1138
41 Y S N I C E R L R S D V Q T S F S I F L 60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
61 H S T V V G F D S K P D E G V Q F S S P 80

FIGURE 46 (cont.)

1199 AAA TGC TCA CAG TCA GAG	gtatataatattttgtttgat	tttttctattcggatagctaata	tatggcag	1272
81 K C S Q S E				86
1273 CTA ATA CGC AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA	1332			
87 L I A N V V K Q M F D E S F E R R R N L	106			
1333 CTG ATG AAA GGG TTT TCC ATG gtaaggattctaattgtgaaatattcac	tgcataactgtttcaaagaga	1405		
107 L M K G F S M		113		
1406 ttgtat	tttaaccgataaag AAT CAT GAA GAT	TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT	1469	
114 N H E D F R A M H V N G V Q N		128		
1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA	1529			
129 D L V S T F P N Y L I S I L E S K N W Q	148			
1530 CTT TTG TTA GAA AT gtaaaataccggtaagatgttgcgcac	tttgaacaagactgacaagtata	1601		
149 L L E I	I G	155		
1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC	1661			
156 S D A M H Y L L S K G S I F E A L P N D	175			
1652 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG	1721			
176 N Y L Q I S G I P L F K N N V F E E T V	195			
1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA	1781			
196 S K K R K R T I E T S I T Q N K S A R K	215			
1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT	1841			
216 E V S W N S I S I S R F S I F Y R S S Y	235			
1842 AAG AAG TTT AAG CAA G gtaactaatactgttatcc	cataactaattttag AT CTA TAT TTT AAC			
1907				
236 K K F K Q D	L Y F N	245		
1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GCA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG	1967			
246 L H S I C D R N T V H M W L Q W I F P R	265			
1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA	2027			
266 Q F G L I N A F Q V K Q L H K V I P L V	285			
2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA	2087			
286 S Q S T V V P K R L L K V Y P L I E Q T	305			
2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT	2147			
306 A K R L H R I S L S K V Y N H Y C P Y I	325			
2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CGG AAC CAG GTG TTT GCG	2207			
326 D T H D D E K I L S Y S L K P N Q V F A	345			
2208 TTT CTT CGA TCC ATT CTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA	2267			
346 F L R S I L V R V F P K L I W G N Q R I	365			
2268 TTT GAG ATA ATA TTA AAA G gtattgtataaaaatttattaccactaacgatttaccag AC CTC GAA ACT	2336			
366 F E I I L K D	L E T	375		

FIGURE 46 (cont.)

2337	TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG	2396	
376	F L K L S R Y E S F S L H Y L M S N I K	395	
2397	gtataatgcacaaattttttaccattaattaacaatcg	ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA	2465
396		I S E I E W L V L G	405
2466	AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG	2525	
406	K R S N A K M C L S D F E K R K Q I F A	425	
2526	GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT	2585	
426	E F I Y W L Y N S F I I P I L Q S F F Y	445	
2586	ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA	2645	
446	I T E S S D L R N R T V Y F R K D I W K	465	
2646	CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA-ATA AAC GAG	2705	
446	L L C R P F I T S M K M E A F E K I N E	485	
2706	gtatTTaaagtatTTTgcAAAAagctaattttcag	AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT	2775
486	N N V R M D T Q K K T	495	
2776	ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG	2835	
496	T L P P A V I R L L P K K N T F R L I T	515	
2836	AAT TTA AGA AAA AGA TTC TTA ATA AAG gtatTTggcatcaatgtactttacttctaattatctatta	2906	
516	N L R K R F L I K	524	
2907	ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG	2967	
525	M G S N K K M L V S T N Q T L R P V	542	
2968	GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG	3027	
543	A S I L K H L I N E E S S G I P F N L E	562	
3028	GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat	3088	
563	V Y M K L L T F K K D L L K H R M F G	581	
3089	tatataatgcgcgattcctcattatTTTgcag	G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA	3155
582	R K K Y F V R I D I	591	
3156	AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC	3215	
592	K S C Y D R I K Q D L M F R I V K K K L	611	
3216	AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT	3275	
612	K D P E F V I R K Y A T I H A T S D R A	631	
3276	ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaatTTtttttcattggaaTTTaaaca	3343	
632	T K N F V S E A F S Y F	643	
3344	atttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA	3405	
644	D M V P F E K V V Q L L S M K T	659	
3406	TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT	3465	
660	S D T L F V D F V D Y W T K S S S E I F	679	
3466	AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtatccaattgtgaattgtataaca	3532	
680	K M L K E H L S G H I V K	692	

FIGURE 46 (cont.)

3533 ctaatgaaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA 693 I G N S Q Y L Q K V G I P Q G S	3593 708
3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG 709 I L S S F L C H F Y M E D L I D E Y L S	3653 728
3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA 729 F T K K K G S V L L R V V D D F L F I T	3713 748
3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagtgctgtcattcc 749 V N K K D A K K F L N L S L R G	3777 764
3778 taagttctaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA 765 F E K H N F S T S L E K T V	3840 778
3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA 779 I N F E N S N G I I N N T F F P N E S K K	3900 798
3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 799 R M P F F G F S V N M R S L D T L L A C	3960 818
3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG 819 P K I D E A L F N S T S V E L T K H M G	4020 838
4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtactaataatagctgacaaataatcg A TCG 839 K S F F Y K I L R	4089 848
4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 849 S L A S F A Q V F I D I T H N S K F N S	4149 868
4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 869 C C N I Y R L G Y S M C M R A Q A Y L K	4209 888
4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtgacttattttactaga 889 R M K D I F I P Q R M F I T D	4274 903
4275 aaagtcatattaatcacccatgg AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 904 L L N V I G R K I W K K L A	4339 917
4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgc 918 E I L G Y T S R R F L S S A E V K W	4401 935
4402 ggtctcgagacttcgacaatattgcacatcg G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 936 L F C L G M R D G L K	4468 946
4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 947 P S F K Y H P C F E Q L I Y Q F Q S L T	4528 966
4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA 967 D L I K P L R P V L R Q V L F L H R R I	4588 986
4589 GCT GAT TAA tgtcattttcaattttatatacatccattttactgggtcttaaacaatttattactaagtata 987 A D *	4665 989

FIGURE 46 (cont.)

FIGURE 47

1 met ser val tyr val val val glu leu leu
 GCCAAGTTCTGCCTGACTGGCTG ATG AGT GTG TAC GTC GTC GAG CTG CTC
 10 20
 arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
 AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG
 30
 leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
 CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT
 40 50
 gly ile arg gln his leu lys arg val gln leu arg glu leu ser
 GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG
 60
 glu ala glu val arg gln his arg glu ala arg pro ala leu leu
 GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG
 70 80
 thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
 ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CGC
 90
 ile val asn met asp tyr val val gly ala arg thr phe arg arg
 ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA
 100 110
 glu lys ala glu arg leu thr ser arg val lys ala leu phe
 GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC
 120
 ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
 AGC GTG CTC AAC TAC GAG CGG GCG CGC CCC GGC CTC CTG GGC
 130 140
 ala ser val leu gly leu asp asp ile his arg ala trp arg thr
 GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC
 150
 phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
 TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC
 160 170
 phe val lys val asp val thr gly ala tyr asp thr ile pro gln
 TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG
 180
 asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
 GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

FIGURE 47 (cont.)

FIGURE 47 (cont.)

390

leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400

ala tyr arg phe his ala cys val leu gln leu pro phe his gln
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

420

gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430

arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

450

val ala gly gly gln gly arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460

arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

480

thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490

pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

510

pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520

his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

540

thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550

arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

560

564
OP
TGA GTGAGTGTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC
CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTCACTTCCCCAC

FIGURE 47 (cont.)

AGGCTGGCGTTCGGTCCACCCAGGGCCAGCTTTCCCTCACCAAGGAGCCGGCTCCACT
CCCCACATAGGAATAGTCATCCCCAGATTGCCATTGTTCACCCCTGCCCTGCCCTCC
TTTGCCCTCCACCCCCCACCATTCAAGGTGGAGACCCCTGAGAAGGACCCCTGGGAGCTTGGG
AATTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCAGGACCCCTGCACCTGGATGGGG
GTCCCTGTGGGTCAAATTGGGGGAGGTGCTGTGGAGTAAAATACTGAATATATGAGTT
TTTCAGTTTGGAAAAAAAAAAAAAAA

FIGURE 48

Motif -1	K
Ep p123	...LVVSLIRCPFFYVTEQQKSYSKT...
Sp Tez1	...FIIPLQSFFYITESSDLRNRT...
Sc Est2	...LIPKIIQTFFYCTEISSTVTIV...
Hs TCP1	...YVVELLRSSFYVTETTFQKNRL...
consensus	FFY TE
Motif 0	p hhh K hR h R
Ep p123	...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...
Sp Tez1	...QKTTLPPAVIRLLPKKN--TFLRLITNLRKRLF...
Sc Est2	...TLSNFNHSKMRIPKKSNNEFRIIAIPCRGAD...
Hs TCP1	...ARPALLTSRSLRFIPKPD--GLRPIVNMDYVVG...
consensus	R PK R I
Motif A	A F
Ep p123	h hDh GY h
Sp Tez1	...PKLFFATMDIEKCYDSVNREKLSTFLK...
Sc Est2	...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
Hs TCP1	...PELYFMKF DVKSCYDSIPRMECMRLIK...
consensus	...PELYFVKV DVTGAYDTIPQDRLTEVIA...//...
F D YD	
Motif B	hPQG pS hh
Ep p123	...NGKFYKOTKGIPQGLCVSSILSSFYYA...
Sp Tez1	...GNSQYQLQKVGVIPQGSILSSFLCHFYME...
Sc Est2	...EDKCYIREDGLFQGSSL SAPIVDLVYD...
Hs TCP1	...RATSYVQCQGIPQGSILSTLLCSLCYG...
consensus	G QG S
Motif C	Y
Ep p123	I F DDhhh
Sp Tez1	...PNVNLLMLRTDDYLLIT TQENN...
Sc Est2	...KKGSVLLRVVDDFLFITVNKKD...
Hs TCP1	...SQDTLILKLADDFLISTDQQQ...
consensus	...RRDGLLLRLVDDFLLVTPHLTH...
	DD L
Motif D	Gh h cK
Ep p123	...NVSRENGFKFNMKKL...
Sp Tez1	...LNLSLRGFEKHNFST...
Sc Est2	...KKLAMGGFQKYNAKA...
Hs TCP1	...LRTLVRGVPEYGCVV...
consensus	G